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PATENT APPLICATION: US/10/038,224

DATE: 01/28/2002
TIME: 17:55:27

Input Set : A:\00033316.txt
Output Set: N:\CRF3\01282002\J038224.raw

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 3 <110> APPLICANT: Schewe et al
 5 <120> TITLE OF INVENTION: Monocotyledon plant cells and plants which synthesise
modified starch
 7 <130> FILE REFERENCE: 514413-3900
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/038,224
C--> 10 <141> CURRENT FILING DATE: 2001-10-19
12 <150> PRIOR APPLICATION NUMBER: DE 10052492.3
13 <151> PRIOR FILING DATE: 2000-10-23
15 <150> PRIOR APPLICATION NUMBER: DE 10064805.3
16 <151> PRIOR FILING DATE: 2000-12-22
18 <160> NUMBER OF SEQ ID NOS: 16
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 5061
24 <212> TYPE: DNA
25 <213> ORGANISM: Solanum tuberosum
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (216)..(4607)
31 <400> SEQUENCE: 1
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36 cgaatttctc gacgcttctt cgctaatttc ctcgttactt cactagaaat cgacgtttct 180
38 agctgaactt gagtgaatta agccagtggg aggat atg agt aat tcc tta ggg    233
39                                       Met Ser Asn Ser Leu Gly
40                                         1               5
42 aat aac ttg ctg tac cag gga ttc cta acc tca aca gtg ttg gaa cat  281
43 Asn Asn Leu Leu Tyr Gln Gly Phe Leu Thr Ser Thr Val Leu Glu His
44             10              15                  20
46 aaa agt aga atc agt cct cct tgt gtt gga ggc aat tct ttg ttt caa  329
47 Lys Ser Arg Ile Ser Pro Pro Cys Val Gly Gly Asn Ser Leu Phe Gln
48         25                  30                  35
50 caa caa gtg atc tcg aaa tca cct tta tca act gag ttt cga ggt aac  377
51 Gln Gln Val Ile Ser Lys Ser Pro Leu Ser Thr Glu Phe Arg Gly Asn
52     40                  45                  50
54 agg tta aag gtg cag aaa aag aaa ata cct atg gga aag aac cgt gct  425
55 Arg Leu Lys Val Gln Lys Lys Lys Ile Pro Met Gly Lys Asn Arg Ala
56 55                  60                  65                  70
59 ttt tct agt tct cct cat gct gta ctt acc act gat acc tct tct gag  473
60 Phe Ser Ser Ser Pro His Ala Val Leu Thr Thr Asp Thr Ser Ser Glu
61                 75                  80                  85
63 cta gca gaa aag ttc agt cta gaa ggg aat att gag cta cag gtt gat  521
64 Leu Ala Glu Lys Phe Ser Leu Glu Gly Asn Ile Glu Leu Gln Val Asp
65             90                  95                  100
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67 gtt agg cct ccc act tca ggt gat gtg tcc ttt gtg gat ttt caa gct    569
68 Val Arg Pro Pro Thr Ser Gly Asp Val Ser Phe Val Asp Phe Gln Ala
69         105                 110                 115
71 aca aat ggt agt gat aaa ctg ttt ttg cac tgg ggg gca gta aag ttc    617
72 Thr Asn Gly Ser Asp Lys Leu Phe Leu His Trp Gly Ala Val Lys Phe
73     120                 125                 130
75 gga aaa gaa aca tgg tct ctt cct aat gat cgt cca gat ggg acc aaa    665
76 Gly Lys Glu Thr Trp Ser Leu Pro Asn Asp Arg Pro Asp Gly Thr Lys
77 135                 140                 145                 150
79 gtg tac aag aac aaa gca ctt aga act cca ttt gtt aaa tct ggc tct    713
80 Val Tyr Lys Asn Lys Ala Leu Arg Thr Pro Phe Val Lys Ser Gly Ser
81             155                 160                 165
83 aac tcc atc ctg aga ctg gag ata cgg gac act gct atc gaa gct att    761
84 Asn Ser Ile Leu Arg Leu Glu Ile Arg Asp Thr Ala Ile Glu Ala Ile
85             170                 175                 180
87 gag ttt ctc ata tac gat gaa gcc tac gat aaa tgg ata aag aat aat    809
88 Glu Phe Leu Ile Tyr Asp Glu Ala Tyr Asp Lys Trp Ile Lys Asn Asn
89         185                 190                 195
91 ggt ggc aat ttt cgt gtc aaa ttg tca aga aaa gag ata cga ggc cca    857
92 Gly Gly Asn Phe Arg Val Lys Leu Ser Arg Lys Glu Ile Arg Gly Pro
93     200                 205                 210
95 gat gtt tca gtt cct gag gag ctt gta cag atc caa tca tat ttg agg    905
96 Asp Val Ser Val Pro Glu Glu Leu Val Gln Ile Gln Ser Tyr Leu Arg
97 215                 220                 225                 230
99 tgg gag agg aag gga aaa cag aat tac acc cct gag aaa gag aag gag    953
100 Trp Glu Arg Lys Gly Lys Gln Asn Tyr Thr Pro Glu Lys Glu Lys Glu
101             235                 240                 245
103 gaa tat gag gct gct cga act gag cta cag gag gaa ata gct cgt ggt   1001
104 Glu Tyr Glu Ala Ala Arg Thr Glu Leu Gln Glu Glu Ile Ala Arg Gly
105             250                 255                 260
107 gct tcc ata cag gac att cga gca agg cta aca aaa act aat gat aaa   1049
108 Ala Ser Ile Gln Asp Ile Arg Ala Arg Leu Thr Lys Thr Asn Asp Lys
109             265                 270                 275
111 agt caa agc aaa gaa gag cct ctt cat gta aca aag agt gaa ata cct   1097
112 Ser Gln Ser Lys Glu Glu Pro Leu His Val Thr Lys Ser Glu Ile Pro
113     280                 285                 290
115 gat gac ctt gcc caa gca caa gct tac att agg tgg gag aaa gca gga   1145
116 Asp Asp Leu Ala Gln Ala Gln Ala Tyr Ile Arg Trp Glu Lys Ala Gly
117 295                 300                 305                 310
120 aag ccg aac tat cct cca gaa aag caa att gaa gaa ctc gaa gaa gca   1193
121 Lys Pro Asn Tyr Pro Pro Glu Lys Gln Ile Glu Glu Leu Glu Glu Ala
122             315                 320                 325
124 aga aga gaa ttg caa ctt gag ctt gag aaa ggc att acc ctt gat gag   1241
125 Arg Arg Glu Leu Gln Leu Glu Leu Glu Lys Gly Ile Thr Leu Asp Glu
126             330                 335                 340
128 ttg cgg aaa aag att aca aaa ggg gag ata aaa act aag gcg gaa aag   1289
129 Leu Arg Lys Lys Ile Thr Lys Gly Glu Ile Lys Thr Lys Ala Glu Lys
130             345                 350                 355
132 cac gtg aaa aga agc tct ttt gcc gtt gaa aga atc caa aga aag aag   1337
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133 His Val Lys Arg Ser Ser Phe Ala Val Glu Arg Ile Gln Arg Lys Lys
134     360             365             370
136 aga gac ttt ggg cag ctt att aat aag tat cct tcc agt cct gca gta     1385
137 Arg Asp Phe Gly Gln Leu Ile Asn Lys Tyr Pro Ser Ser Pro Ala Val
138 375             380             385             390
140 caa gta caa aag gtc ttg gaa gaa cca cca gcc tta tct aaa att aag     1433
141 Gln Val Gln Lys Val Leu Glu Glu Pro Pro Ala Leu Ser Lys Ile Lys
142             395             400             405
144 ctg tat gcc aag gag aag gag gag cag att gat gat ccg atc ctt aat     1481
145 Leu Tyr Ala Lys Glu Lys Glu Glu Gln Ile Asp Asp Pro Ile Leu Asn
146             410             415             420
148 aaa aag atc ttt aag gtc gat gat ggg gag cta ctg gta ctg gta gca     1529
149 Lys Lys Ile Phe Lys Val Asp Asp Gly Glu Leu Leu Val Leu Val Ala
150         425             430             435
152 aag tcc tct ggg aag aca aaa gta cat ata gct aca gat ctg aat cag     1577
153 Lys Ser Ser Gly Lys Thr Lys Val His Ile Ala Thr Asp Leu Asn Gln
154         440             445             450
156 cca att act ctt cac tgg gca tta tcc aaa agt cgt gga gag tgg atg     1625
157 Pro Ile Thr Leu His Trp Ala Leu Ser Lys Ser Arg Gly Glu Trp Met
158 455             460             465             470
160 gta cca cct tca agc ata ttg cct cct gga tca att att tta gac aag     1673
161 Val Pro Pro Ser Ser Ile Leu Pro Pro Gly Ser Ile Ile Leu Asp Lys
162             475             480             485
164 gct gcc gaa aca cct ttt tcc gcc agt tct tct gat ggt cta act tct     1721
165 Ala Ala Glu Thr Pro Phe Ser Ala Ser Ser Ser Asp Gly Leu Thr Ser
166             490             495             500
168 aag gta caa tct ttg gat ata gta att gaa gat ggc aat ttt gtg ggg     1769
169 Lys Val Gln Ser Leu Asp Ile Val Ile Glu Asp Gly Asn Phe Val Gly
170         505             510             515
172 atg cca ttt gtt ctt ttg tct ggt gaa aaa tgg att aag aac caa ggg     1817
173 Met Pro Phe Val Leu Leu Ser Gly Glu Lys Trp Ile Lys Asn Gln Gly
174         520             525             530
176 tcg gat ttc tat gtt gac ttc agt gct gca tcc aaa tta gca ctc aag     1865
177 Ser Asp Phe Tyr Val Asp Phe Ser Ala Ala Ser Lys Leu Ala Leu Lys
178 535             540             545             550
181 gct gct ggg gat ggc agt gga act gca aag tct tta ctg gat aaa ata     1913
182 Ala Ala Gly Asp Gly Ser Gly Thr Ala Lys Ser Leu Leu Asp Lys Ile
183             555             560             565
185 gca gat atg gaa agt gag gct cag aag tca ttt atg cac cgg ttt aat     1961
186 Ala Asp Met Glu Ser Glu Ala Gln Lys Ser Phe Met His Arg Phe Asn
187             570             575             580
189 att gct gct gac ttg ata gaa gat gcc act agt gct ggt gaa ctt ggt     2009
190 Ile Ala Ala Asp Leu Ile Glu Asp Ala Thr Ser Ala Gly Glu Leu Gly
191         585             590             595
193 ttt act gga att ctt gta tgg atg agg ttc atg gct aca agg caa ctg     2057
194 Phe Thr Gly Ile Leu Val Trp Met Arg Phe Met Ala Thr Arg Gln Leu
195         600             605             610
197 ata tgg aac aaa aac tat aac gta aaa cca cgt gaa ata agc aag gct     2105
198 Ile Trp Asn Lys Asn Tyr Asn Val Lys Pro Arg Glu Ile Ser Lys Ala
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199 615                     620                     625                     630
201 cag gac aga ctt aca gac ttg ttg cag aat gct ttc acc agt cac cct   2153
202 Gln Asp Arg Leu Thr Asp Leu Leu Gln Asn Ala Phe Thr Ser His Pro
203                     635                     640                     645
205 caa tac cgt gaa att ttg cgg atg att atg tca act gtt gga cgt gga   2201
206 Gln Tyr Arg Glu Ile Leu Arg Met Ile Met Ser Thr Val Gly Arg Gly
207                     650                     655                     660
209 ggt gaa ggg gat gta gga cag cga att agg gat gaa att ttg gtc atc   2249
210 Gly Glu Gly Asp Val Gly Gln Arg Ile Arg Asp Glu Ile Leu Val Ile
211             665                     670                     675
213 cag agg aaa aat gac tgc aag ggt ggt atg atg gaa gaa tgg cat cag   2297
214 Gln Arg Lys Asn Asp Cys Lys Gly Gly Met Met Glu Glu Trp His Gln
215     680                     685                     690
217 aaa ttg cat aat aat act agt cct gat gat gtt gtg atc tgt cag gca   2345
218 Lys Leu His Asn Asn Thr Ser Pro Asp Asp Val Val Ile Cys Gln Ala
219 695                     700                     705                     710
221 ttg att gac tac atc aag agt gat ttt gat ctt ggt gtt tat tgg aaa   2393
222 Leu Ile Asp Tyr Ile Lys Ser Asp Phe Asp Leu Gly Val Tyr Trp Lys
223                     715                     720                     725
225 acc ctg aat gag aac gga ata aca aaa gag cgt ctt ttg agt tat gac   2441
226 Thr Leu Asn Glu Asn Gly Ile Thr Lys Glu Arg Leu Leu Ser Tyr Asp
227             730                     735                     740
229 cgt gct atc cat tct gaa ccg aat ttt aga gga gat caa aag aat ggt   2489
230 Arg Ala Ile His Ser Glu Pro Asn Phe Arg Gly Asp Gln Lys Asn Gly
231             745                     750                     755
233 ctt ttg cgt gat tta ggt cac tat atg aga aca ttg aag gct gtt cat   2537
234 Leu Leu Arg Asp Leu Gly His Tyr Met Arg Thr Leu Lys Ala Val His
235     760                     765                     770
237 tca ggt gca gat ctt gag tct gct att gca aac tgc atg ggc tac aaa   2585
238 Ser Gly Ala Asp Leu Glu Ser Ala Ile Ala Asn Cys Met Gly Tyr Lys
239 775                     780                     785                     790
242 act gag gga gaa ggc ttt atg gtt gga gtc cag ata aat cct gta tca   2633
243 Thr Glu Gly Glu Gly Phe Met Val Gly Val Gln Ile Asn Pro Val Ser
244             795                     800                     805
246 ggc ttg cca tct ggc ttt cag ggc ctc ctc cat ttt gtc tta gac cat   2681
247 Gly Leu Pro Ser Gly Phe Gln Gly Leu Leu His Phe Val Leu Asp His
248             810                     815                     820
250 gtg gaa gat aaa aat gtg gaa act ctt ctt gag gga ttg cta gag gct   2729
251 Val Glu Asp Lys Asn Val Glu Thr Leu Leu Glu Gly Leu Leu Glu Ala
252             825                     830                     835
254 cgt gag gag ctt agg ccc ttg ctt ctc aaa cca aac aac cgt cta aag   2777
255 Arg Glu Glu Leu Arg Pro Leu Leu Leu Lys Pro Asn Asn Arg Leu Lys
256     840                     845                     850
258 gat ctg ctg ttt ttg gac ata gca ctt gat tct aca gtt aga aca gca   2825
259 Asp Leu Leu Phe Leu Asp Ile Ala Leu Asp Ser Thr Val Arg Thr Ala
260 855                     860                     865                     870
262 gta gaa agg gga tat gaa gaa ttg aac aac gct aat cct gag aaa atc   2873
263 Val Glu Arg Gly Tyr Glu Glu Leu Asn Asn Ala Asn Pro Glu Lys Ile
264             875                     880                     885
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266 atg tac ttc atc tcc ctc gtt ctt gaa aat ctc gca ctc tct gtg gac   2921
267 Met Tyr Phe Ile Ser Leu Val Leu Glu Asn Leu Ala Leu Ser Val Asp
268         890                 895                 900
270 gat aat gaa gat ctt gtt tat tgc ttg aag gga tgg aat caa gct ctt   2969
271 Asp Asn Glu Asp Leu Val Tyr Cys Leu Lys Gly Trp Asn Gln Ala Leu
272         905                 910                 915
274 tca atg tcc aat ggt gga gac aac cat tgg gct tta ttt gca aaa gct   3017
275 Ser Met Ser Asn Gly Gly Asp Asn His Trp Ala Leu Phe Ala Lys Ala
276     920                 925                 930
278 gta ctt gac aga atc cgt ctt gca ctt gca agc aag gca gag tgg tac   3065
279 Val Leu Asp Arg Ile Arg Leu Ala Leu Ala Ser Lys Ala Glu Trp Tyr
280 935                 940                 945                 950
282 cat cac tta ttg cag cca tct gcc gaa tat cta gga tca atc ctt ggg   3113
283 His His Leu Leu Gln Pro Ser Ala Glu Tyr Leu Gly Ser Ile Leu Gly
284                 955                 960                 965
286 gtg gac caa tgg gct ttg aac ata ttt act gaa gaa att ata cgt gct   3161
287 Val Asp Gln Trp Ala Leu Asn Ile Phe Thr Glu Glu Ile Ile Arg Ala
288                 970                 975                 980
290 gga tca gca gct tca tta tcc tct ctt ctt aat aga ctc gat ccc gtg   3209
291 Gly Ser Ala Ala Ser Leu Ser Ser Leu Leu Asn Arg Leu Asp Pro Val
292             985                 990                 995
294 ctt cgg aaa act gca aat cta gga agt tgg cag att atc agt cca gtt   3257
295 Leu Arg Lys Thr Ala Asn Leu Gly Ser Trp Gln Ile Ile Ser Pro Val
296     1000                1005                1010
298 gaa gcc gtt gga tat gtt gtc gtt gtg gat gag ttg ctt tca gtt cag   3305
299 Glu Ala Val Gly Tyr Val Val Val Val Asp Glu Leu Leu Ser Val Gln
300 1015                1020                1025                1030
303 aat gaa atc tac aag aag ccc acg atc tta gta gca aac tct gtt aaa   3353
304 Asn Glu Ile Tyr Lys Lys Pro Thr Ile Leu Val Ala Asn Ser Val Lys
305                 1035                1040                1045
307 gga gag gag gaa att cct gat ggt gct gtt gcc ctg ata aca cca gac   3401
308 Gly Glu Glu Glu Ile Pro Asp Gly Ala Val Ala Leu Ile Thr Pro Asp
309             1050                1055                1060
311 atg cca gat gtt ctt tca cat gtt tct gtt cga gct aga aat ggg aag   3449
312 Met Pro Asp Val Leu Ser His Val Ser Val Arg Ala Arg Asn Gly Lys
313         1065                1070                1075
315 gtt tgc ttt gct aca tgc ttt gat ccc aat ata ttg gct gac ctc caa   3497
316 Val Cys Phe Ala Thr Cys Phe Asp Pro Asn Ile Leu Ala Asp Leu Gln
317     1080                1085                1090
319 gca aag gaa gga agg att ttg ctc tta aag cct aca cct tca gac ata   3545
320 Ala Lys Glu Gly Arg Ile Leu Leu Leu Lys Pro Thr Pro Ser Asp Ile
321 1095                1100                1105                1110
323 atc tat agt gag gtg aat gag att gag ctc caa agt tca agt aac ttg   3593
324 Ile Tyr Ser Glu Val Asn Glu Ile Glu Leu Gln Ser Ser Ser Asn Leu
325                 1115                1120                1125
327 gta gaa gct gaa act tca gca aca ctt aga ttg gtg aaa aag caa ttt   3641
328 Val Glu Ala Glu Thr Ser Ala Thr Leu Arg Leu Val Lys Lys Gln Phe
329             1130                1135                1140
331 ggt ggt tgt tac gca ata tca gca gat gaa ttc aca agt gaa atg gtt   3689
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L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date